

logo

NTDB id 1384 A4U84 RS08525 WP 010787006.1
NTDB id 235827 CEP45 RS05625 WP 265490391.1
NTDB id 1366 NTHI RS01950 WP 011271972.1
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NTDB id 1251 GC085 RS07725 WP 011946523.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
NTDB id 1058 ABD1 RS01615 WP 001274986.1
consensus

MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQALEKAKKKFKQDIVPYLIDNFSISPLTIAETIISLEFGPELLDLGVDFPALF
MSALHTSPKFTGFFRRLLVEEKHLSAATMQTALLDAAKRAKQDITVAYLIEEVHLSPSLLAETIIISAEFAEYPFDLDVYDTSIQI

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QKNCEEKQLLLRRLAVPVQETEHKLLWLVADDDENNLTACEIFAFMTHKQIEPVVIAASDELKYLLNALSPQEQPIYEES.. 100
 QNNQQKYPQLLLRRLAVPVQEDSTTLWLAIESLNNIRGCETFSFLTGKIVPEVVGQFGLKQLLQALNPQNDAIYAVAK.. 99
 QRNQQQSSQLLLRRLAVPLKEENNRLWLGVDLSLSNLSACETIAFITGKPVPEILLESSQLKELLQQLTPHQMQVEE.... 102
 ERNQQQSSQLLLRRLAVPLKEENNRLWLGVDLSLSNLSACETIAFITGKPVPEILLESSQLKELLQQLTPNQMQVEE.... 102
 CQQLGLRELITRYPDALPIAKQGNLLLVAVSDPTLLQAEEFRFATGLQVELALADHRAALQAAIRRLYGRSISGAANQGK.. 151
 CQQLGLRELITRHNALPLHRTPSTLLWLVADPTNQQAEDDFRATGLQVELVLADFRELSTAIRRLYGRSISGKESGLK.. 151
 CQTLGLRDLITRHNALPLNRSTSLILAVADPTNLQAEDDFRATGLQVELVLADFRELTAAIRRLYGRSISGKESGLK.. 151
 PVNLVNEKLIKRRHAMVPLFSRGTNLYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE.. 160
 LKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMD AIRFNSKLLKVEPIIVVHDKLERLLSEHFVEETHFNFDTE.. 158
 PKDLVDQKLILKHLRLPLIQRGQILYVATSNPSNIEAIDAIRFNSKLLVEPVIIVHHKLEKVLGQHFAEESFFDNDE.. 158
 **** !***** ** !***** ** !***** ** !***** ** !***** ** !***** ** !***** **

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Position	Sequence	Score
1	LAFLV.EQ	165
2	ENTLYEPQSD	171
3	QVKFYQHQS	170
4	QVKFYQHQS	170
5	EISQDELANL	230
6	EINQEELASL	230
7	EINQDELAGL	230
8	DSGDLEGL	239
9	ELD	234
10	EFD	234

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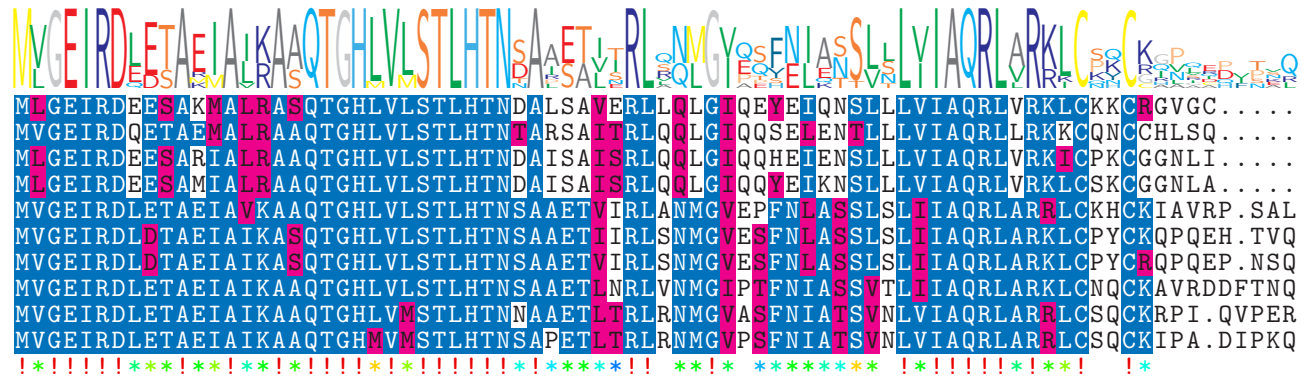
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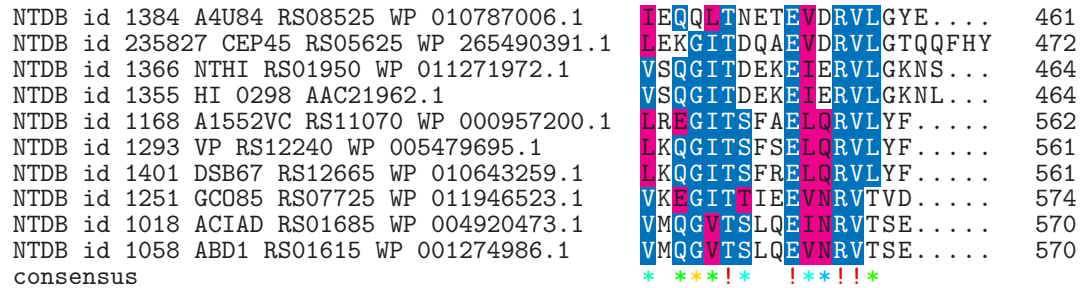
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X	non conserved
X	similar
X	$\geq 50\%$ conserved